

Preliminary results of a genome scan of Marchigiana cattle typed by a Illumina 54,000 SNP panel

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Carcass yield (CY) is an important trait for producers and processing industries, however selection indices are difficult to estimate and use since measurements are possible only post mortem. Selection on DNA polymorphisms affecting CY could allow choosing live animals even at very early age.



228 Marchigiana intact bulls raised in similar conditions were slaughtered at age of 500-700 days. Carcass yield was recorded and adjusted for age at slaughter. DNA was extracted, normalized and genotyped for the Illumina 54k SNP panel. SNPs and animals with missing>1% were excluded as well as SNPs with MAF<5%.

Model to analyse SNP effect on CY

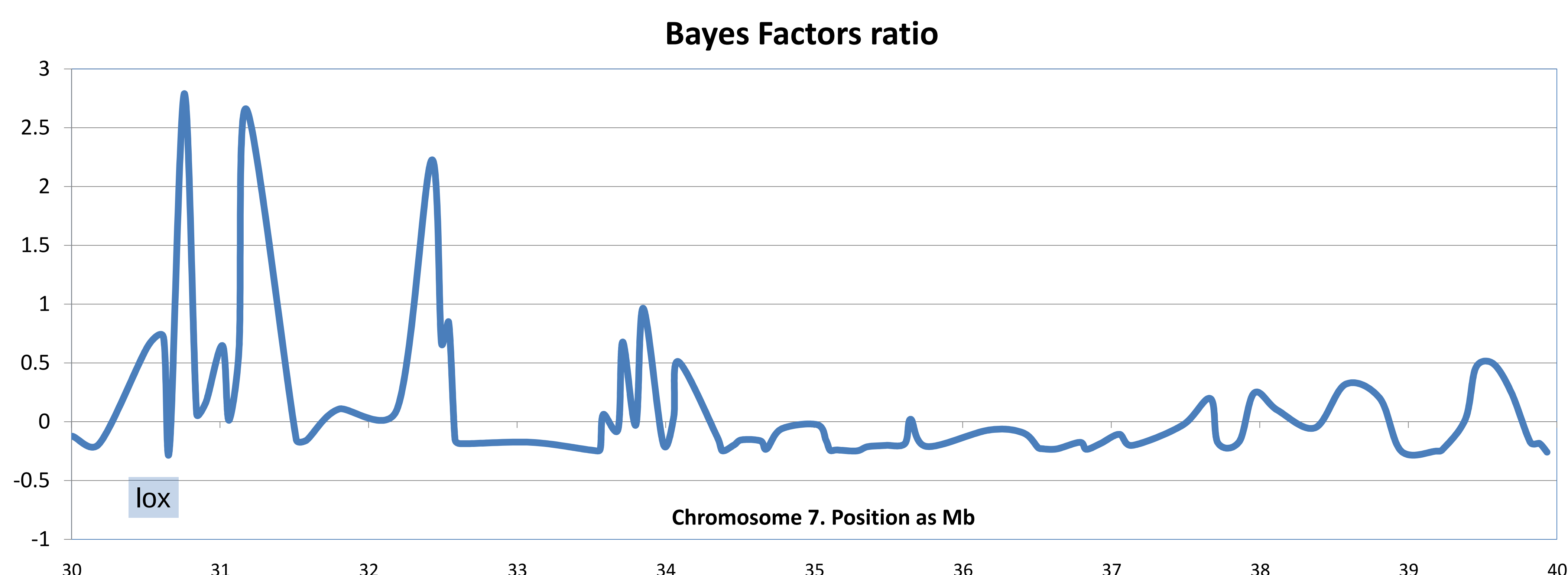
$$Y_i = \mu + AX_i + DI(X_i = 1) + \varepsilon_i \quad (1)$$

Y_i denotes the phenotype for individual i , X_i the genotype for individual i (coded as 0, 1 or 2), A the additive effect, D the dominance effect, and ε an error term (assumed to be iid normal). Y was quantile-transformed as $H(Y) = e^{1+Y} + (5 + Y)^2$ to obtain a normal distribution within classes of genotypes.

$$BF = \frac{\Pr(D|M_2)}{\Pr(D|M_1)} = \frac{\int \Pr(\theta_2|M_2) \Pr(D|\theta_2, M_2) d\theta_2}{\int \Pr(\theta_1|M_1) \Pr(D|\theta_1, M_1) d\theta_1}$$

Effect of a single SNP on the trait was estimated by computing the Bayes Factors (BF) relative to model (1) versus $Y_i = \mu + \varepsilon_i$ using BimBam software (Servin & Stephens, 2007). P-values were computed by applying 100,000 permutations.

Only 12 SNPs showed a BF ratio>2. Of these, three belong to chromosome 7 and are located close to the region of lysyl oxidase (LOX), which has been reported to be implicated in several meat characteristics. Their P-values range from $2e^{-5}$ to $8e^{-5}$. The two SNPs on chromosome 7 with lowest P-value are significant also after a Bonferroni correction. High values of additive component are associated with high P-values, while dominance effects are negligible.



These preliminary data need to be improved by: increasing the individuals sampled, correcting for multiple comparisons, testing for haplotypes or clusters of adjacent SNPs.

Servin, B and Stephens M. Imputation-based analysis of association studies: candidate genes and quantitative traits. PLoS Genetics, 3(7): e114, 2007.

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